

SPECIFICATION AMENDMENTS

The paragraph on page 59, line 19 to page 60, line 13 has been amended as follows

The ORF of the MN cDNA shown in Figures 1A-1C have the coding capacity for a 459 amino acid protein with a calculated molecular weight of 49.7 kd. MN protein has an estimated pI of about 4. As assessed by amino acid sequence analysis, the deduced primary structure of the MN protein can be divided into four distinct regions. The initial hydrophobic region of 37 amino acids (AA) corresponds to a signal peptide. The mature protein has an N-terminal part of 377 AA, a hydrophobic transmembrane segment of 20 AA and a C-terminal region of 25 AA. Alternatively, the MN protein can be viewed as having five domains as follows: (1) a signal peptide [amino acids (AA) 1-37; SEQ. ID. NO.: 6]; (2) a region of homology to collagen alpha1 chain (AA 38-135; SEQ. ID. NO.: 50); (3) a carbonic anhydrase domain (AA 136-391; SEQ. ID. NO.: 51); (4) a transmembrane region (AA ~~414-433~~ 415-434; SEQ. ID. NO.: 52); and (5) an intracellular C terminus (AA 435-459; SEQ. ID. NO.: 53). (The AA numbers are keyed to Figures 1A-1C.)

The information for SEQ ID NO: 28 in Sequence Listing has been amended as follows

(

2) INFORMATION FOR SEQ ID NO: 28:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: ~~415~~ **445** base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(A) DESCRIPTION: 1st MN exon

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

~~ACAGTCAGCC GCATGGCTCC CCTGTGCCCC AGCCCCTGGC TCCCTCTGTT GATCCCGGCC 60~~
~~CCTGCTCCAG GCCTCACTGT GCAACTGCTG CTGTCACTGC TGCTTCTGGT GCCTGTCCAT 120~~
~~CCCCAGAGGT TCCCCCGGAT GCAGGAGGAT TCCCCCTTGG GAGGAGGCTC TTCTGGGGAA 180~~
~~GATGACCCAC TGGGCGAGGA GGATCTGCCC AGTGAAGAGG ATTCACCCAG AGAGGAGGAT 240~~
~~CCACCCGGAG AGGAGGATCT ACCTGGAGAG GAGGATCTAC CTGGAGAGGA GGATCTACCT 300~~
~~GAAGTTAAGC CTAAATCAGA AGAAGAGGGC TCCCTGAAGT TAGAGGATCT ACCTACTGTT 360~~
~~GAGGCTCCTG GAGATCCTCA AGAACCCAG AATAATGCCC ACAGGGACAA ACAAG 415~~

GCCCGTACAC ACCGTGTGCT GGGACACCCC ACAGTCAGCC GCATGGCTCC CCTGTGCCCC 60
AGCCCCTGGC TCCCTCTGTT GATCCCGGCC CCTGCTCCAG GCCTCACTGT GCAACTGCTG 120
CTGTCACTGC TGCTTCTGGT GCCTGTCCAT CCCCAGAGGT TCCCCCGGAT GCAGGAGGAT 180
TCCCCCTTGG GAGGAGGCTC TTCTGGGGAA GATGACCCAC TGGGCGAGGA GGATCTGCCC 240
AGTGAAGAGG ATTCACCCAG AGAGGAGGAT CCACCCGGAG AGGAGGATCT ACCTGGAGAG 300
GAGGATCTAC CTGGAGAGGA GGATCTACCT GAAGTTAAGC CTAAATCAGA AGAAGAGGGC 360

TCCCTGAAGT TAGAGGATCT ACCTACTGTT GAGGCTCCTG GAGATCCTCA AGAACCCAG 420
AATAATGCCC ACAGGGACAA AGAAG 445

The information for SEQ ID NO: 52 in the Sequence Listing has
been amended as follows

(2) INFORMATION FOR SEQ ID NO: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(A) DESCRIPTION: transmembrane region

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

~~Asp Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val~~
~~1 5 10 15~~

~~Ala Phe Leu Val~~
~~20~~

Ile Leu Ala Leu Val Phe Gly Leu Leu Phe Ala Val Thr Ser Val Ala
1 5 10 15

Phe Leu Val Gln
20